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AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Original) A genetic marker, which exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM.

2. (Original) The genetic marker as set forth in Claim 1, wherein the Gramineae plant is a Hordeum or Triticum.

3. (Original) The genetic marker as set forth in Claim 2, wherein the Hordeum or Triticum is barley.

4. (Original) The genetic marker as set forth in Claim 3, wherein the genomic DNA is 2H chromosome.

5. (Currently Amended) The genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 4~~, wherein the genetic marker is for being amplified with a first primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 1, and a primer having the base sequence of S.E.Q. ID. NO. 2.

6. (Original) The genetic marker as set forth in Claim 5, being distanced from the Fusarium head blight-resistance factor by approximately 0cM.

7. (Currently Amended) The genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 4~~, wherein the genetic marker is for being amplified with a second primer set that is a combination

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of a primer having the base sequence of S.E.Q. ID. NO. 3, and a primer having the base sequence of S.E.Q. ID. NO. 4.

8. (Original) The genetic marker as set forth in Claim 7, being distanced from the Fusarium head blight-resistance factor by approximately 0.6cM.

9. (Original) The genetic marker as set forth in Claim 8, wherein the Genetic marker has the base sequence of S.E.Q. ID. NO. 8 or 9.

10. (Currently Amended) The genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 4~~, wherein the genetic marker is ~~for being~~ amplified with a sixth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 22, and a primer having the base sequence of S.E.Q. ID. NO. 23.

11. (Currently Amended) The genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 4~~, wherein the genetic marker is for being amplified with a seventh primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 24, and a primer having the base sequence of S.E.Q. ID. NO. 25.

12. (Currently Amended) The genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 4~~, wherein the genetic marker is for being amplified with an eighth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 26, and a primer having the base sequence of S.E.Q. ID. NO. 27.

13. (Original) The genetic marker as set forth in Claim 3, wherein the genomic DNA is 5H chromosome.

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14. (Currently Amended) The genetic marker as set forth in Claim 1~~Claim 1, 2, or 13~~, wherein the genetic marker is for being amplified with a third primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 5, and a primer having the base sequence of S.E.Q. ID. NO. 6.

15. (Original) The genetic marker as set forth in Claim 14, being distanced from the Fusarium head blight-resistance factor by approximately 9cM.

16. (Original) The genetic marker as set forth in Claim 15, wherein the genetic marker has the base sequence of S.E.Q. ID. NO. 10 or 11.

17. (Currently Amended) The genetic marker as set forth in Claim ~~1, 2, or 13~~, wherein the genetic marker is for being amplified with a fourth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 5, and a primer having the base sequence of S.E.Q. ID. NO. 7.

18. (Original) The genetic marker as set forth in Claim 17, being distanced from the Fusarium head blight-resistance factor by approximately 9cM.

19. (Original) The genetic marker as set forth in Claim 18, wherein the genetic marker has the base sequence of S.E.Q. ID. NO. 12 or 13.

20. (Currently Amended) The genetic marker as set forth in Claim ~~1, 2, 3, or 13~~, wherein: amplification of the genetic marker is carried out by:

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

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(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a fifth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 21, and a primer having the base sequence of S.E.Q. ID. NO. 20.

21. (Currently Amended) The genetic marker as set forth in Claim 13 ~~or 20~~, being distanced from the Fusarium head blight-resistance factor by approximately 2.2cM.

22. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 13~~, wherein the genetic marker is for being amplified with a ninth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 28, and a primer having the base sequence of S.E.Q. ID. NO. 29.

23. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 13~~, wherein the genetic marker is for being amplified with a tenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 30, and a primer having the base sequence of S.E.Q. ID. NO. 31.

24. (Original) The genetic marker as set forth in Claim 3, wherein the genomic DNA is 4H chromosome.

25. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 24~~, wherein: amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment

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obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using an eleventh primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 32, and a primer having the base sequence of S.E.Q. ID. NO. 33.

26. (Currently Amended) The genetic marker as set forth in Claim 1,~~2,3, or 24~~, wherein: amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a twelfth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 34, and a primer having the base sequence of S.E.Q. ID. NO. 35.

27. (Currently Amended) The genetic marker as set forth in Claim 1,~~2,3, or 24~~, wherein: amplification of the genetic marker is carried out by

(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

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(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a thirteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 36, and a primer having the base sequence of S.E.Q. ID. NO. 37.

28. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 24~~, wherein the genetic marker is for being amplified with a fourteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 38, and a primer having the base sequence of S.E.Q. ID. NO. 39.

29. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 24~~, wherein the genetic marker is for being amplified with a fifteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 40, and a primer having the base sequence of S.E.Q. ID. NO. 41.

30. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 24~~, wherein the genetic marker is for being amplified with a sixteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 42, and a primer having the base sequence of S.E.Q. ID. NO. 43.

31. (Original) The genetic marker as set forth in Claim 3, wherein the genomic DNA is 6H chromosome.

32. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 31~~, wherein: amplification of the genetic marker is carried out by

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(a) ligating MseI adaptors having the base sequences of S.E.Q. ID. NOs. 16 and 17 and EcoRI adaptors having the base sequences of S.E.Q. ID. NOs. 14 and 15 to a DNA fragment obtained by digesting a genomic DNA of a Gramineae plant with restriction enzymes MseI and EcoRI,

(b) performing pre-amplification of the ligated DNA fragment by using MseI universal primer having the base sequence of S.E.Q. ID. NO. 19, and EcoRI universal primer having the base sequence of S.E.Q. ID. NO. 18, and

(c) amplifying the pre-amplified fragment by using a seventeenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 44, and a primer having the base sequence of S.E.Q. ID. NO. 45.

33. (Currently Amended) The genetic marker as set forth in Claim 1, ~~2, 3, or 31~~, wherein the genetic marker is for being amplified with an eighteenth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 46, and a primer having the base sequence of S.E.Q. ID. NO. 47.

34. (Currently Amended) A DNA fragment isolating method, comprising:
isolating, by using the genetic marker as set forth in Claim 1 ~~any one of Claims 1 to 33~~, a DNA fragment including a Fusarium head blight-resistance factor.

35. (Original) A method for producing a Fusarium head blight-resistance plant, comprising:
introducing, into a genomic DNA of a plant, the DNA fragment that is obtained by the method as set forth in Claim 34 and includes the Fusarium head blight-resistance factor.

36. (Currently Amended) A method ~~The genetic marker~~ as set forth in Claim 35, wherein the plant is Gramineae.

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37. (Currently Amended) A method~~The genetic marker~~ as set forth in Claim 36, wherein the Gramineae plant is Hordeum or Triticum.

38. (Currently Amended) A method~~The genetic marker~~ as set forth in Claim 37, wherein the Hordeum or Triticum is barley.

39. (Currently Amended) A Fusarium head blight-resistant plant obtained by the method as set forth in Claim 35~~any one of Claims 35 to 38~~.

40. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

detecting the genetic marker as set forth in Claim 1~~any one of Claims 1 to 33~~.

41. (Currently Amended) A kit for judging~~by the method as set forth in Claim 40~~, whether a plant is a Fusarium head blight-resistant plant or not, said kit having a means for detecting a genetic marker which exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM.

42. (Currently Amended) A gene detecting apparatus, comprising a genetic marker which exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM, wherein at least one of the genetic markers as set forth in Claim 1~~Claims 1 to 33~~ is fixed.

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43. (Currently Amended) A primer population for use in detecting the genetic markers as set forth in Claim 1 ~~Claims 1 to 33~~, comprising:

at least two ~~of~~ primers having the base sequences of S.E.Q. ID. NOs. 1 to 7, and 20 to 47.

44. (Original) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms on one or more of the genetic markers that exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM and wherein the genetic markers are:

(a) amplified with a first primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 1, and a primer having the base sequence of S.E.Q. ID. NO. 2 or

(b) amplified with a second primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 3, and a primer having the base sequence of S.E.Q. ID. NO. 4, or a combination of (a) and (b) as set forth in ~~Claims 5 and 7~~, respectively.

45. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of ~~a~~the genetic markers as set forth in Claim 1 ~~Claims 11 and 12~~, respectively.

46. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of a polymorphism of the genetic marker as set forth in Claim 14 ~~or 17~~, and a polymorphism of the genetic marker as set forth in Claim 20.

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47. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of ~~the~~ genetic markers as set forth in Claim 22~~Claims 22 and 23~~, respectively.

48. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claim 25~~Claims 25 and 26~~, respectively.

49. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of ~~the~~ genetic markers as set forth in Claim 27~~Claims 27 and 28~~, respectively.

50. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claim 29~~Claims 29 and 30~~, respectively.

51. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

performing detection of polymorphisms of the genetic markers as set forth in Claim 32~~Claims 32 and 33~~, respectively.

52. (Currently Amended) A method for judging whether a plant is a Fusarium head blight-resistant plant or not, comprising:

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performing detection of polymorphisms on one or more of the genetic markers that exists in a genomic DNA of a Gramineae plant and is linked to a Fusarium head blight-resistance factor, wherein:

a distance from the Fusarium head blight-resistance factor to the Genetic marker is within a range of approximately 0 to 10cM and wherein the genetic markers are:

(a) amplified with a second primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 3, and a primer having the base sequence of S.E.Q. ID. NO. 4 or

(b) amplified with a sixth primer set that is a combination of a primer having the base sequence of S.E.Q. ID. NO. 22, and a primer having the base sequence of S.E.Q. ID. NO. 23, or a combination of (a) and b) as set forth in Claims 7 and 10, respectively.